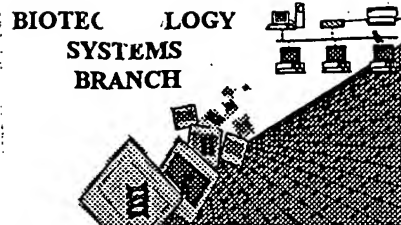


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/088,594
Source: PCT10
Date Processed by STIC: 3/28/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 01/29/2002



Does Not Comply PCT10
Corrected Diskette Needed

Errors on pp. 2 + 7

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002
TIME: 10:30:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
5 <120> TITLE OF INVENTION: Novel Transaldolase
7 <130> FILE REFERENCE: 11236WO1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/088,594
C--> 10 <141> CURRENT FILING DATE: 2002-03-21
12 <150> PRIOR APPLICATION NUMBER: JP 99/266548
13 <151> PRIOR FILING DATE: 1999-09-21
15 <160> NUMBER OF SEQ ID NOS: 3
17 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
20 <211> LENGTH: 360
21 <212> TYPE: PRT
22 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
24 <400> SEQUENCE: 1

length should be 1080!
*A coding sequence is always a nucleic sequence.
Thus, response can only be DNA or RNA.*

26	atg tct cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc	48
27	Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu	
28	1 5 10 15	
30	gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt	96
31	Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val	
32	20 25 30	
34	att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc	144
35	Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe	
36	35 40 45	
38	gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag	192
39	Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu	
40	50 55 60	
42	ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc	240
43	Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser	
44	65 70 75 80	
46	atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag	288
47	Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu	
48	85 90 95	
50	tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt	336
51	Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg	
52	100 105 110	
54	atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg	384
55	Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp	
56	115 120 125	
58	gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca	432

RAW SEQUENCE LISTING

DATE: 03/28/2002

PATENT APPLICATION: US/10/088,594

TIME: 10:30:26

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60      130      135      140
62 ggt tct ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt 480
63 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
64 145      150      155      160
66 aac gtc acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct 528
67 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
68      165      170      175
70 gcg tac atc gag gga atc aag cag gca gct gca aac ggc cac gac gta 576
71 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
72      180      185      190
74 tcc aag atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt 624
75 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
76      195      200      205
78 gag atc gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct 672
79 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
80      210      215      220
82 ctg cgc ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg 720
83 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
84 225      230      235      240
86 tac aag gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act 768
87 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
88      245      250      255
90 cag cgc cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct 816
91 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
92      260      265      270
94 gca act ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc 864
95 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
96      275      280      285
98 atg cca gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac 912
99 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
100      290      295      300
102 ggt gac acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc 960
103 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
104 305      310      315      320
106 cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg 1008
107 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
108      325      330      335
110 gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt 1056
111 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
112      340      345      350
E--> 114 gag tcc atg gaa gct cgc ctg aag 1080!
E--> 115 Glu Ser Met Glu Ala Arg Leu Lys
E--> 116 355 360 — number misaligned
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 4108
164 <212> TYPE: DNA
165 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
167 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING

DATE: 03/28/2002

PATENT APPLICATION: US/10/088,594

TIME: 10:30:26

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Output Set: N:\CRF3\03282002\J088594.raw

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170 <221> NAME/KEY: CDS
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176 ttgcaccgta ttgcttgccg aacatttttc ttttcctttc ggtttttcga gaattttcac 120
178 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacaccttt gacacatttg 180
180 aaccacagtt ggttataaaa tgggttcaac atcactatgg ttagagggtg tgacgggtca 240
182 gattaagcaa agactacttt cggggttagat cacctttgcc aaatttgaat caattaacct 300
184 aagtcgtaga tctgatcatc ggatctaacy aaaacgaacc aaaactttgg tcccggttta 360
186 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
187 Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
188 1 5 10
190 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct 459
191 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
192 15 20 25
194 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc 507
195 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
196 30 35 40 45
198 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc 555
199 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
200 50 55 60
202 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca 603
203 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
204 65 70 75
206 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag 651
207 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
208 80 85 90
210 tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg 699
211 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
212 95 100 105
214 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac 747
215 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
216 110 115 120 125
218 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt 795
219 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
220 130 135 140
222 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc 843
223 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
224 145 150 155
226 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac 891
227 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
228 160 165 170
230 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct 939
231 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
232 175 180 185
234 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg 987
235 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
236 190 195 200 205

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TIME: 10:30:26

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238 ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct 1035
239 Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala
240      210      215      220
242 ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc 1083
243 Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr
244      225      230      235
246 att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg 1131
247 Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val
248      240      245      250
250 gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc 1179
251 Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg
252      255      260      265
254 acc atc atc ggc ttc cca gct cca acc atg atg aac acc ggt gct gtg 1227
255 Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val
256 270      275      280      285
258 cac ggt gct gct ctt ggc gca gct gag gtt gca gca acc aag act gag 1275
259 His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu
260      290      295      300
262 ctt gga ttc gat cct gag gct cac ttc gcg atc gac gat gag gtt atc 1323
263 Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile
264      305      310      315
266 gct cac acc cgc tcc ctc gca gag cgc gct gca cag aag aag gct gca 1371
267 Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala
268      320      325      330
270 tgg cag gtc aag ttc gat gag tgg gca gct gcc aac cct gag aac aag 1419
271 Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys
272      335      340      345
274 gct ctg ttc gat cgc ctg aac tcc cgt gag ctt cca gcg ggc tac gct 1467
275 Ala Leu Phe Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala
276 350      355      360      365
278 gac gag ctc cca aca tgg gat gca gat gag aag ggc gtc gca act cgt 1515
279 Asp Glu Leu Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg
280      370      375      380
282 aag gct tcc gag gct gca ctt cag gca ctg ggc aag acc ctt cct gag 1563
283 Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu
284      385      390      395
286 ctg tgg ggc ggt tcc gct gac ctc gca ggt tcc aac aac acc gtg atc 1611
287 Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile
288      400      405      410
290 aag ggc tcc cct tcc ttc ggc cct gag tcc atc tcc acc gag acc tgg 1659
291 Lys Gly Ser Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp
292      415      420      425
294 tct gct gag cct tac ggc cgt aac ctg cac ttc ggt atc cgt gag cac 1707
295 Ser Ala Glu Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His
296 430      435      440      445
298 gct atg gga tcc atc ctc aac ggc att tcc ctc cac ggt ggc acc cgc 1755
299 Ala Met Gly Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg
300      450      455      460
302 cca tac ggt gga acc ttc ctc atc ttc tcc gac tac atg cgt cct gca 1803

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002

TIME: 10:30:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\03282002\J088594.raw

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303 Pro Tyr Gly Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala
304      465      470      475
306 gtt cgt ctt gca gct ctc atg gag acc gac gct tac tac gtc tgg acc 1851
307 Val Arg Leu Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr
308      480      485      490
310 cac gac tcc atc ggt ctg ggc gaa gat ggc cca acc cac cag cct gtt 1899
311 His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val
312      495      500      505
314 gaa acc ttg gct gcg ctg cgc gcc atc cca ggt ctg tcc gtc ctg cgt 1947
315 Glu Thr Leu Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg
316 510      515      520      525
318 cct gca gat gcg aat gag acc gcc cag gct tgg gct gca gca ctt gag 1995
319 Pro Ala Asp Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu
320      530      535      540
322 tac aag gaa ggc cct aag ggt ctt gca ctg acc cgc cag aac gtt cct 2043
323 Tyr Lys Glu Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro
324      545      550      555
326 gtt ctg gaa ggc acc aag gag aag gct gct gaa ggc gtt cgc cgc ggt 2091
327 Val Leu Glu Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly
328      560      565      570
330 ggc tac gtc ctg gtt gag ggt tcc aag gaa acc cca gat gtg atc ctc 2139
331 Gly Tyr Val Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu
332      575      580      585
334 atg ggc tcc ggc tcc gag gtt cag ctt gca gtt aac gct gcg aaa gct 2187
335 Met Gly Ser Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala
336 590      595      600      605
338 ctg gaa gct gag ggc gtt gca gct cgc gtt gtt tca gtt cct tgc atg 2235
339 Leu Glu Ala Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met
340      610      615      620
342 gat tgg ttc cag gag cag gac gca gag tac atc gag tcc gtt ctg cct 2283
343 Asp Trp Phe Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro
344      625      630      635
346 gca gct gtg acc gct cgt gtg tct gtt gaa gct ggc atc gca atg cct 2331
347 Ala Ala Val Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro
348      640      645      650
350 tgg tac cgc ttc ttg ggc acc cag ggc cgt gct gtc tcc ctt gag cac 2379
351 Trp Tyr Arg Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His
352      655      660      665
354 ttc ggt gct tct gcg gat tac cag acc ctg ttt gag aag ttc ggc atc 2427
355 Phe Gly Ala Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile
356 670      675      680      685
358 acc acc gat gca gtc gtg gca gcg gcc aag gac tcc att aac agt 2472
359 Thr Thr Asp Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Ser
360      690      695      700
362 taattgccct gctgttttta gcttcaaccc ggggcagtat gattctcogg aattttattg 2532
364 ccccggttg ttgttgtaa tcggtacaaa ggggtcttaag cacatccctt acttgccctgc 2592
366 tctccttgag cacagttcaa gaacaattct ttttaaggaaa atttagtttc atg tct 2648
367      Met Ser

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W--> 368

1

OK.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002

TIME: 10:30:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\03282002\J088594.raw

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369 cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac 2696
370 His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp
W--> 371      5      10      15
373 ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt att gag 2744
374 Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu
W--> 375      20      25      30
377 gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc gca gca 2792
378 Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala
W--> 379      35      40      45      50
381 gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag ctc aag 2840
382 Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys
W--> 383      55      60      65
385 gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc atc gac 2888
386 Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp
W--> 387      70      75      80
389 gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc 2936
390 Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser
W--> 391      85      90      95
393 aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct 2984
394 Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser
W--> 395     100     105     110
397 gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag 3032
398 Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys
W--> 399    115     120     125     130
401 gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca ggt tct 3080
402 Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser
W--> 403     135     140     145
405 ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc 3128
406 Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val
W--> 407     150     155     160
409 acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg tac 3176
410 Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Tyr
W--> 411     165     170     175
413 atc gag gga atc aag cag gca gct gca aac ggc cac gac gta tcc aag 3224
414 Ile Glu Gly Ile Lys Gln Ala Ala Asn Gly His Asp Val Ser Lys
W--> 415     180     185     190
417 atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc 3272
418 Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile
W--> 419    195     200     205     210
421 gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc 3320
422 Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg
W--> 423     215     220     225
425 ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag 3368
426 Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys
W--> 427     230     235     240
429 gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc 3416
430 Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg
W--> 431     245     250     255
433 cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct gca act 3464

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002

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437 ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca 3512
438 Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro
W--> 439 275      280      285      290
441 gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac ggt gac 3560
442 Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His Gly Asp
W--> 443      295      300      305
445 acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt 3608
446 Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu
W--> 447      310      315      320
449 gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc 3656
450 Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr
W--> 451      325      330      335
453 gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt gag tcc 3704
454 Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser
W--> 455      340      345      350
457 atg gaa gct cgc ctg aag tagaatcagc acgctgcac agtaacggcg 3752
458 Met Glu Ala Arg Leu Lys
W--> 459 355      360
461 acatgaaatc gaattagttc gatcttatgt ggccgttaca catctttcat taaagaaagg 3812
463 atcgtgacgc taccatcgtg agcacaaaaca cgacccccctc cagctggaca aacccactgc 3872
465 gcgaccgcga ggataaacga ctccccgcga tcgctggccc ttccggcatg gtgatcttcg 3932
467 gtgtcactgg cgacttggtc cgaagggaagc tgctccccgc catttatgat ctagcaaacc 3992
469 gcggattgct gccccagga ttctcgttgg taggttacgg ccgcgcgaa tgggtccaaag 4052
471 aagactttga aaaatacgta cgcgatgccg caagtgtctg tgctcgtacg gaattc 4108
E--> 476 18/12

```

-delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002

TIME: 10:30:27

Input Set : A:\EP.txt

Output Set: N:\CRF3\03282002\J088594.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:115 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:116 M:252 E: No. of Seq. differs, <211>LENGTH:Input:360 Found:368 SEQ:1
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:476 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:4109 SEQ:3
L:476 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:476 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4108 Found:4109 SEQ:3